

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bard, Jonathan A
Borowsky, Beth
Smith, Kelli E

(ii) TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 65

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 52241-E/JPW/KDB

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212 278 0400
(B) TELEFAX: 212 391 0525

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 63..1172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCTCCAGCC TAGGCGTTCT ACCTGGAAGA ATGCAGGGGC CCAGTACCTA GGACTGAGGA	60
AG ATG GCT GAC ATC CAG AAC ATT TCG CTG GAC AGC CCA GGG AGC GTA	107

Met Ala Asp Ile Gln Asn Ile Ser Leu Asp Ser Pro Gly Ser Val	1	5	10	15	
GGG GCT GTG GCA GTG CCT GTG ATC TTT GCC CTC ATC TTC CTG TTG GGC					155
Gly Ala Val Ala Val Pro Val Ile Phe Ala Leu Ile Phe Leu Leu Gly	20	25	30		
ATG GTG GGC AAT GGG CTG GTG TTG GCT GTG CTA CTG CAG CCT GGC CCA					203
Met Val Gly Asn Gly Leu Val Leu Ala Val Leu Leu Gln Pro Gly Pro	35	40	45		
AGT GCC TGG CAG GAG CCA AGC AGT ACC ACA GAT CTC TTC ATC CTC AAC					251
Ser Ala Trp Gln Glu Pro Ser Ser Thr Thr Asp Leu Phe Ile Leu Asn	50	55	60		
TTG GCC GTG GCC GAC CTT TGC TTC ATC CTG TGC TGC GTG CCC TTC CAG					299
Leu Ala Val Ala Asp Leu Cys Phe Ile Leu Cys Cys Val Pro Phe Gln	65	70	75		
GCA GCC ATC TAC ACA CTG GAT GCC TGG CTC TTT GGG GCT TTC GTG TGC					347
Ala Ala Ile Tyr Thr Leu Asp Ala Trp Leu Phe Gly Ala Phe Val Cys	80	85	90	95	
AAG ACG GTA CAT CTG CTC ATC TAC CTC ACC ATG TAT GCC AGC AGC TTC					395
Lys Thr Val His Leu Leu Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe	100	105	110		
ACC CTG GCG GCC GTC TCC CTG GAC AGG TAC CTG GCT GTG CGG CAC CCA					443
Thr Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala Val Arg His Pro	115	120	125		
CTG CGC TCC AGA GCC CTG CGC ACC CCG CGC AAC GCG CGC GCC GCC GTG					491
Leu Arg Ser Arg Ala Leu Arg Thr Pro Arg Asn Ala Arg Ala Ala Val	130	135	140		
GGG CTC GTG TGG CTG CTG GCG GCT CTC TTT TCC GCG CCC TAC CTA AGC					539
Gly Leu Val Trp Leu Leu Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser	145	150	155		
TAT TAC GGC ACG GTG CGC TAC GGC GCG CTC GAG CTC TGC GTG CCC GCT					587
Tyr Tyr Gly Thr Val Arg Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala	160	165	170	175	
TGG GAG GAC GCG CGG CGG CGC GCG CTG GAC GTG GCC ACC TTC GCC GCG					635
Trp Glu Asp Ala Arg Arg Ala Leu Asp Val Ala Thr Phe Ala Ala	180	185	190		
GGC TAC CTG CTG CCG GTG GCC GTG GTG AGC CTG GCC TAC GGA CGC ACG					683
Gly Tyr Leu Leu Pro Val Ala Val Val Ser Leu Ala Tyr Gly Arg Thr	195	200	205		
CTA TGT TTC CTA TGG GCC GCC GTG GGT CCC GCG GGC GCG GCG GCA GCA					731
Leu Cys Phe Leu Trp Ala Ala Val Gly Pro Ala Gly Ala Ala Ala Ala	210	215	220		
GAG GCG CGC AGA CGG GCG ACC GGC CGG GCG GGA CGC CGC GCC ATG CTG GCA					779
Glu Ala Arg Arg Arg Ala Thr Gly Arg Ala Gly Arg Ala Met Leu Ala	225	230	235		
GTG GCC GCG CTC TAC GCG CTT TGC TGG GGC CCG CAC CAC GCG CTC ATC					827
Val Ala Ala Leu Tyr Ala Leu Cys Trp Gly Pro His His Ala Leu Ile	240	245	250	255	

CTC TGC TTC TGG TAC GGC CGC TTC GCC TTC AGC CCG GCC ACC TAC GCC Leu Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala 260 265 270	875
TGT CGC CTG GCC TCG CAC TGC CTC GCC TAC GCC AAC TCC TGC CTT AAC Cys Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn 275 280 285	923
CCG CTC GTC TAC TCG CTC GCC TCG CGC CAC TTC CGC GCG CGC TTC CGC Pro Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg 290 295 300	971
CGC CTG TGG CCC TGC GGC CGT CGC CGC CAC CGC CAC CAC CGC GCT Arg Leu Trp Pro Cys Gly Arg Arg His Arg His His Arg Ala 305 310 315	1019
CAT CGA GCC CTC CGT CGT GTC CAG CCG GCG TCT TCG GGC CCC GCC GGT His Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly 320 325 330 335	1067
TAT CCC GGC GAC GCC AGG CCT CGT GGT TGG AGT ATG GAG CCC AGA GGG Tyr Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly 340 345 350	1115
GAT GCT CTG CGT GGT GGT GGA GAG ACT AGA CTA ACC CTG TCC CCC AGG Asp Ala Leu Arg Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg 355 360 365	1163
GGA CCT CAA TAACCTGCC CGCTTGGACT CTGACGTCTG TCAGAATGCC Gly Pro Gln 370	1212
ACCAAGGAAC ATCTAGGGAA CGGCAGTCTC GCCAGGCTCC ACCAAAAAGC AGAAGCAAAG TTGCAGGG	1272
	1280

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asp Ile Gln Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly 1 5 10 15
Ala Val Ala Val Pro Val Ile Phe Ala Leu Ile Phe Leu Leu Gly Met 20 25 30
Val Gly Asn Gly Leu Val Leu Ala Val Leu Leu Gln Pro Gly Pro Ser 35 40 45
Ala Trp Gln Glu Pro Ser Ser Thr Thr Asp Leu Phe Ile Leu Asn Leu 50 55 60
Ala Val Ala Asp Leu Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala 65 70 75 80

Ala Ile Tyr Thr Leu Asp Ala Trp Leu Phe Gly Ala Phe Val Cys Lys
85 90 95

Thr Val His Leu Leu Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe Thr
100 105 110

Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala Val Arg His Pro Leu
115 120 125

Arg Ser Arg Ala Leu Arg Thr Pro Arg Asn Ala Arg Ala Ala Val Gly
130 135 140

Leu Val Trp Leu Leu Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser Tyr
145 150 155 160

Tyr Gly Thr Val Arg Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala Trp
165 170 175

Glu Asp Ala Arg Arg Ala Leu Asp Val Ala Thr Phe Ala Ala Gly
180 185 190

Tyr Leu Leu Pro Val Ala Val Val Ser Leu Ala Tyr Gly Arg Thr Leu
195 200 205

Cys Phe Leu Trp Ala Ala Val Gly Pro Ala Gly Ala Ala Ala Glu
210 215 220

Ala Arg Arg Arg Ala Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val
225 230 235 240

Ala Ala Leu Tyr Ala Leu Cys Trp Gly Pro His His Ala Leu Ile Leu
245 250 255

Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys
260 265 270

Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro
275 280 285

Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg
290 295 300

Leu Trp Pro Cys Gly Arg Arg His Arg His His Arg Ala His
305 310 315 320

Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly Tyr
325 330 335

Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly Asp
340 345 350

Ala Leu Arg Gly Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg Gly
355 360 365

Pro Gln
370

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1417 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAC TCA GCG ATG ACT TTG GCT CTG CTC TCC CCT CCT CCA TCT CCC ACG	48
His Ser Ala Met Thr Leu Ala Leu Leu Ser Pro Pro Pro Ser Pro Thr	
375 380 385	
AGC TTC CAG CCC AGA ACA CCT GGC CAG ACC CAG GTC GGG GGA GTT AGA	96
Ser Phe Gln Pro Arg Thr Pro Gly Gln Thr Gln Val Gly Gly Val Arg	
390 395 400	
TCC CGG GGT CAA GCA ACC AGA ACT GGG GGC TCT TGC CTG AGG ATT CCA	144
Ser Arg Gly Gln Ala Thr Arg Thr Gly Ser Cys Leu Arg Ile Pro	
405 410 415	
GCT TCT CTT CCC AGG TGC CCG TCT GAT GGG GAG ATG GCT GAT GCC CAG	192
Ala Ser Leu Pro Arg Cys Pro Ser Asp Gly Glu Met Ala Asp Ala Gln	
420 425 430	
AAC ATT TCA CTG GAC AGC CCA GGG AGT GTG GGG GCC GTG GCA GTG CCT	240
Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly Ala Val Ala Val Pro	
435 440 445 450	
G TG GTC TTT GCC CTA ATC TTC CTG CTG GGC ACA GTG GGC AAT GGG CTG	288
Val Val Phe Ala Leu Ile Phe Leu Leu Gly Thr Val Gly Asn Gly Leu	
455 460 465	
G TG CTG GCA GTG CTC CTG CAG CCT GGC CCG AGT GCC TGG CAG GAG CCT	336
Val Leu Ala Val Leu Leu Gln Pro Gly Pro Ser Ala Trp Gln Glu Pro	
470 475 480	
G GC AGC ACC ACG GAC CTG TTC ATC CTC AAC CTG GCG GTG GCT GAC CTC	384
Gly Ser Thr Thr Asp Leu Phe Ile Leu Asn Leu Ala Val Ala Asp Leu	
485 490 495	
TGC TTC ATC CTG TGC GTG CCC TTC CAG GCC ACC ATC TAC ACG CTG	432
Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala Thr Ile Tyr Thr Leu	
500 505 510	
G AT GCC TGG CTC TTT GGG GCC CTC GTC TGC AAG GCC GTG CAC CTG CTC	480
Asp Ala Trp Leu Phe Gly Ala Leu Val Cys Lys Ala Val His Leu Leu	
515 520 525 530	
A TC TAC CTC ACC ATG TAC GCC AGC AGC TTT ACG CTG GCT GCT GTC TCC	528
Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe Thr Leu Ala Ala Val Ser	
535 540 545	
G TG GAC AGG TAC CTG GCC GTG CGG CAC CCG CTG CGC TCG CGC GCC CTG	576
Val Asp Arg Tyr Leu Ala Val Arg His Pro Leu Arg Ser Arg Ala Leu	
550 555 560	
C GC ACG CCG CGT AAC GCC CGC GCC GCA GTG GGG CTG GTG TGG CTG CTG	624

Arg Thr Pro Arg Asn Ala Arg Ala Ala Val Gly Leu Val Trp Leu Leu	
565 570 575	
GCG GCG CTC TTC TCG GCG CCC TAC CTC AGC TAC TAC GGC ACC GTG CGC	672
Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser Tyr Tyr Gly Thr Val Arg	
580 585 590	
TAC GGC GCG CTG GAG CTC TGC GTG CCC GCC TGG GAG GAC GCG CGC CGC	720
Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala Trp Glu Asp Ala Arg Arg	
595 600 605 610	
CGC GCC CTG GAC GTG GCC ACC TTC GCT GCC GGC TAC CTG CTG CCC GTG	768
Arg Ala Leu Asp Val Ala Thr Phe Ala Ala Gly Tyr Leu Leu Pro Val	
615 620 625	
GCT GTG GTG AGC CTG GCC TAC GGG CGC ACG CTG CGC TTC CTG TGG GCC	816
Ala Val Val Ser Leu Ala Tyr Gly Arg Thr Leu Arg Phe Leu Trp Ala	
630 635 640	
GCC GTG GGT CCC GCG GGC GCG GCG GCG GCG GAG GCG CGG CGG AGG GCG	864
Ala Val Gly Pro Ala Gly Ala Ala Ala Glu Ala Arg Arg Arg Arg Ala	
645 650 655	
ACG GGC CGC GCG GGG CGC GCC ATG CTG GCG GTG GCC GCG CTC TAC GCG	912
Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val Ala Ala Leu Tyr Ala	
660 665 670	
CTC TGC TGG GGT CCG CAC CAC GCG CTC ATC CTG TGC TTC TGG TAC GGC	960
Leu Cys Trp Gly Pro His His Ala Leu Ile Leu Cys Phe Trp Tyr Gly	
675 680 685 690	
CGC TTC GCC TTC AGC CCG GCC ACC TAC GCC TGC CGC CTG GCC TCA CAC	1008
Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys Arg Leu Ala Ser His	
695 700 705	
TGC CTG GCC TAC GCC AAC TCC TGC CTC AAC CCG CTC GTC TAC GCG CTC	1056
Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro Leu Val Tyr Ala Leu	
710 715 720	
GCC TCG CGC CAC TTC CGC GCG CGC TTC CGC CGC CTG TGG CCG TGC GGC	1104
Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg Leu Trp Pro Cys Gly	
725 730 735	
CGC CGA CGC CGC CAC CGT GCC CGC CGC GCC TTG CGT CGC GTC CGC CCC	1152
Arg Arg Arg Arg His Arg Ala Arg Arg Ala Leu Arg Arg Val Arg Pro	
740 745 750	
GCG TCC TCG GGC CCA CCC GGC TGC CCC GGA GAC GCC CGG CCT AGC GGG	1200
Ala Ser Ser Gly Pro Pro Gly Cys Pro Gly Asp Ala Arg Pro Ser Gly	
755 760 765 770	
AGG CTG CTG GCT GGT GGC GGC CAG GGC CCG GAG CCC AGG GAG GGA CCC	1248
Arg Leu Leu Ala Gly Gly Gly Gln Gly Pro Glu Pro Arg Glu Gly Pro	
775 780 785	
GTC CAC GGC GGA GAG GCT GCC CGA GGA CCG GAA TAAACCCTGC CGCCTGGACT	1301
Val His Gly Gly Glu Ala Ala Arg Gly Pro Glu	
790 795	
CCGCCTGTGT CCGTCTGTCT CACTCCCGTT CTCCGAAGGC GGGACGCCAC CGGGGCCAGGG	1361
ATGGGGCAAT GCCACGAGCT CTCTGAGGGG CGTTGAGTGG AGCGACTTGT CCCCCGC	1417

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 427 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

His Ser Ala Met Thr Leu Ala Leu Leu Ser Pro Pro Pro Ser Pro Thr
1 5 10 15

Ser Phe Gln Pro Arg Thr Pro Gly Gln Thr Gln Val Gly Gly Val Arg
20 25 30

Ser Arg Gly Gln Ala Thr Arg Thr Gly Gly Ser Cys Leu Arg Ile Pro
35 40 45

Ala Ser Leu Pro Arg Cys Pro Ser Asp Gly Glu Met Ala Asp Ala Gln
50 55 60

Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly Ala Val Ala Val Pro
65 70 75 80

Val Val Phe Ala Leu Ile Phe Leu Leu Gly Thr Val Gly Asn Gly Leu
85 90 95

Val Leu Ala Val Leu Gln Pro Gly Pro Ser Ala Trp Gln Glu Pro
100 105 110

Gly Ser Thr Thr Asp Leu Phe Ile Leu Asn Leu Ala Val Ala Asp Leu
115 120 125

Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala Thr Ile Tyr Thr Leu
130 135 140

Asp Ala Trp Leu Phe Gly Ala Leu Val Cys Lys Ala Val His Leu Leu
145 150 155 160

Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe Thr Leu Ala Ala Val Ser
165 170 175

Val Asp Arg Tyr Leu Ala Val Arg His Pro Leu Arg Ser Arg Ala Leu
180 185 190

Arg Thr Pro Arg Asn Ala Arg Ala Ala Val Gly Leu Val Trp Leu Leu
195 200 205

Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser Tyr Tyr Gly Thr Val Arg
210 215 220

Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala Trp Glu Asp Ala Arg Arg
225 230 235 240

Arg Ala Leu Asp Val Ala Thr Phe Ala Ala Gly Tyr Leu Leu Pro Val
245 250 255

Ala Val Val Ser Leu Ala Tyr Gly Arg Thr Leu Arg Phe Leu Trp Ala
260 265 270

Ala Val Gly Pro Ala Gly Ala Ala Ala Glu Ala Arg Arg Arg Ala
275 280 285

Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val Ala Ala Leu Tyr Ala
290 295 300

Leu Cys Trp Gly Pro His His Ala Leu Ile Leu Cys Phe Trp Tyr Gly
305 310 315 320

Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys Arg Leu Ala Ser His
325 330 335

Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro Leu Val Tyr Ala Leu
340 345 350

Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg Leu Trp Pro Cys Gly
355 360 365

Arg Arg Arg Arg His Arg Ala Arg Arg Ala Leu Arg Arg Val Arg Pro
370 375 380

Ala Ser Ser Gly Pro Pro Gly Cys Pro Gly Asp Ala Arg Pro Ser Gly
385 390 395 400

Arg Leu Leu Ala Gly Gly Gln Gly Pro Glu Pro Arg Glu Gly Pro
405 410 415

Val His Gly Gly Glu Ala Ala Arg Gly Pro Glu
420 425

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Leu Ala Pro Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro
1 5 10 15

Glu Pro Pro Ala Glu Pro Arg Pro Leu Phe Gly Ile Gly Val Glu Asn
20 25 30

Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val Leu
35 40 45

Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly Lys
50 55 60

Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala Asp
65 70 75 80

Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr Ala
85 90 95

Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His Tyr

100	105	110
Phe Phe Thr Val Ser Met Leu Val Ser Ile Phe Thr Leu Ala Ala Met		
115	120	125
Ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg Ser Ser Ser		
130	135	140
Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe Ile Trp Ala		
145	150	160
Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr Tyr Gln Arg Leu Phe		
165	170	175
His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu His Trp Pro Asn Gln		
180	185	190
Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe Gly Tyr Leu		
195	200	205
Leu Pro Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val Leu Asn His		
210	215	220
Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu Ala Ser Lys		
225	230	240
Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val Phe Gly Ile		
245	250	255
Ser Trp Leu Pro His His Val Ile His Leu Trp Ala Glu Phe Gly Ala		
260	265	270
Phe Pro Leu Thr Pro Ala Ser Phe Phe Phe Arg Ile Thr Ala His Cys		
275	280	285
Leu Ala Tyr Ser Asn Ser Ser Val Asn Pro Ile Ile Tyr Ala Phe Leu		
290	295	300
Ser Glu Asn Phe Arg Lys Ala Tyr Lys Gln Val Phe Lys Cys Arg Val		
305	310	320
Cys Asn Glu Ser Pro His Gly Asp Ala Lys Glu Lys Asn Arg Ile Asp		
325	330	335
Thr Pro Pro Ser Thr Asn Cys Thr His Val		
340	345	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGTACCCCT ATTTTCGCG CTCATCTTCC TCGTGGGCAC CGTGG

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGCACCGCCA GCACCAGCGC GTTGCCACG GTGCCACGA GGAAG

45

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCAGCACCAAC CAACCTGTTCAATCCTCAACC TGGGCGTGGC CGACCTGTGT

50

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCCTGGAAA GGCACGCAGC ACAGGGATGAA ACACAGGTCTG GCCACGCCA

50

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGCAAGGCT GTTCATTCC TCATCTTCT CACTATGCAC GCCAG

45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAGACGGCG GCCAGCGTGA AGCTGCTGGC GTGCATAGTG AGAAA

45

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AACCGCGTGG CCGCCATCGG GCTCATCTGG GGGCTAGCAC TGCTC

45

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGTAGCTCAG GTAGGGCCCG GAGAAGAGCA GTGCTAGCCC CCAGA

45

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCCCATGGAC CTCTGCACCT TCGTCTTTAG CTACCTGCTG CCAGT

45

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCATAGGTC AGACTGAGGA CTAGCACTGG CAGCAGGTAG CTAAA

45

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCATCATC GTGGCGGTGC TTTTCTGCCT CTGTTGGATG CCCCA

45

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACACGCAG AGGATAAGCG CGTGGTGGGG CATCCAACAG AGGCA

45

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTGCGCATC CTTTCACACC TAGTTCCCTA TGCCAACTCC TGTGT

45

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGACCAGAGC GTAAACGATG GGGTTGACAC AGGAGTTGGC ATAGGA

46

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTCAGTGAA GGGAAATGGGA GCGA

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTAGTGTATA AACTTGCAGA TGAAGGC

27

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAATGGCT CCGGCAGCCA GGG

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGCAGAGCA GCGAGCCGAA CAC

23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCTGACATC CAGAACATTG CGCT

24

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAGATGTACC GTCTTGACAA CGAA

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CATCTGCTCA TCTACCTCAC CATG

24

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATAGGAAAC ATAGCGTGCG TCCG

24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTTCTAG AGATCCCTCG ACCTC

25

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGGCGCAGAA CTGGTAGGTA TGGAA

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCTCATCCTC TGCTTCTGGT ACG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
CAGATGTACC GTCTTGCACA CGAA

24

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGAGGGATCCC AACTTTGCCT CTGCTTTTG GTGG

34

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCTCAGTGAA GGGAAATGGGA GCGA

24

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTTGCTTGTA CGCCTTCCGG AAGT

24

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGGGCAACAG CCTAGTGATC ACCG

24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTGCTCCCAG CAGAAGGTCT GGTT

24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGAATGGCT CCGGCAGCCA GGG

23

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTGGAGACCA GAGCGTAAAC GATGG

25

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGATGGCTGA CATCCAGAAC ATTCGCTGG ACAGCCCAGG GAGCG

45

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATCACAGGCA CTGCCACAGC CCCTACGCTC CCTGGGCTGT CCAGCG

46

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGGCTGATG CCCAGAACAT TTCAC

25

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AGCCAGGCAT CCAGCGTGTA GAT

23

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACGGTCGCTT CGCCTTCAGC CCGGCCACCT ACGCCTGTCG CCTGG

45

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACGGTCGCTT CGCCTTCAGC CCGGCCACCT ACGCCTGTCG CCTGG

45

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCGCAACGCG CGCGCCGCCG TGGGGCTCGT GTGGCTGCTG GCGGC

45

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTACACGC TGGATGCCCTG GCTCTTGCG GCCCTCGTCT GCAAG

45

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATCTACACGC TGGATGCCCT GGCT

24

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGTAGCGCAC GGTGCCGTAG TA

22

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATGGATCCG CCACCATGGC TGATGCCAG AACATTCAC

40

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAGGTACCT GTCCACGGAG ACAGCAGC

28

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATGGCTGAT GCCCAGAAC A TTTCACTGGA CAGCCCAGGG AGTGT

45

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GACCACAGGC ACTGCCACGG CCCCCACACT CCCTGGGCTG TCCAG

45

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGCAGCCTGG CCCAAGTGCC TGGCAGGAGC CAAGCAGTAC CACAG

45

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGCGGATCCA TTATGTCTGC ACTCCGAAGG AAATTTG

37

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGCGAATTCT TATGTGAAGC GATCAGAGTT CATTTC

38

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCAGGGATCCG CTATGGCTGG TGATTCTAGG AATG

34

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCGGAATTCC CCTCACACCG AGCCCCTGG

29

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCAAGCTTCT AATACGACTC ACTATAGGGC CACCATGGCT GATGCCAGA

50

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTGAGG GTTTATTCCG GTCCTCG

57

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TCAGCGGCAC CATGAACGTC TCGGGCT

27

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGCCACATCA ACCGTCAGGA TGCT

24

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATGGCTGATG CCCAGAACAT TTCAC

25

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAGCGCACGG TGCCGTAGTA GCTGAGGT

28

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGAAAGGGT CCCTCCTGCT GCTGCT

26

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TATCAGCTCC ATGCCCTCTA GAAGCC

26

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Jonathan A. Bard, et al.
Serial No. : 09/058,333
Filed : April 9, 1998
For : DNA ENCODING GALANIN GALR3 RECEPTOR AND USES
THEREOF

1185 Avenue of the Americas
New York, New York 10036
August 3, 1998

Assistant Commissioner for Patents
Washington, D.C. 20231
Box: Missing Parts

Sir:

STATEMENT IN ACCORDANCE WITH 37 C.F.R. §1.821(f)

In accordance with 37 C.F.R. §1.821(f), I hereby certify that the computer readable form containing the nucleic acid and/or amino acid sequences required by 37 C.F.R. §1.821(e) and submitted in connection with the above-identified application, has the same information as replacement pages 171-194 of the subject application entitled "Sequence Listing."

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these were made with the knowledge that wilful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such wilful false statements may jeopardize the validity of the application or any patent issued thereon.

Respectfully submitted,



Kimberly D. Branch
c/o Cooper & Dunham LLP
1185 Avenue of the Americas
New York, New York 10036
(212) 278-0400

Applicants: Jonathan A. Bard et al.
Serial No.: Not Yet Known
Filed: Herewith
Exhibit 3

ATCC

10801 University Blvd • Manassas, VA 20110-2209 • Telephone: 703-365-2700 • FAX: 703-

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT ISSUED PURSUANT TO RULE 7.3
AND VIABILITY STATEMENT ISSUED PURSUANT TO RULE 10.2

To: (Name and Address of Depositor or Attorney)

Cooper & Dunham LLP
Attn: John P. White, Esq.
1185 Avenue of the Americas
New York, NY 10036

COPY

Deposited on Behalf of: Synaptic Pharmaceutical Corporation (Docket 52241-E)

Identification Reference by Depositor: ATCC Designation

Plasmid M67 209708

The deposit was accompanied by: a scientific description a proposed taxonomic description indicated above.

The deposit was received March 27, 1998 by this International Depository Authority and has been accepted.

AT YOUR REQUEST: We will inform you of requests for the strain for 30 years.

The strain will be made available if a patent office signatory to the Budapest Treaty certifies one's right to receive, or if a U.S. Patent is issued citing the strain, and ATCC is instructed by the United States Patent & Trademark Office or the depositor to release said strain.

If the culture should die or be destroyed during the effective term of the deposit, it shall be your responsibility to replace it with living culture of the same.

The strain will be maintained for a period of at least 30 years from date of deposit, or five years after the most recent request for a sample, whichever is longer. The United States and many other countries are signatory to the Budapest Treaty.

The viability of the culture cited above was tested April 8, 1998. On that date, the culture was viable.

International Depository Authority: American Type Culture Collection, Manassas, VA 20110-2209 USA.

Signature of person having authority to represent ATCC:

Barbara M. Hailey
Barbara M. Hailey, Administrator, Patent Depository

Date: April 22, 1998

cc: Kimberly Branch

Applicants: Jonathan A. Bard et al.
Serial No.: Not Yet Known
Filed: Herewith
Exhibit 4